

SEQUENCE SUBMISSION

SEQ ID NO: 1 provides primate IL-1 ζ nucleotide sequence.
SEQ ID NO: 2 provides primate IL-1 ζ polypeptide sequence.
5 SEQ ID NO: 3 provides primate IL-1 ζ variant nucleotide sequence.
SEQ ID NO: 4 provides primate IL-1 ζ variant polypeptide sequence.
SEQ ID NO: 5 provides primate IL-1 α polypeptide sequence.
SEQ ID NO: 6 provides rodent IL-1 α polypeptide sequence.
SEQ ID NO: 7 provides primate IL-1 γ polypeptide sequence.
10 SEQ ID NO: 8 provides rodent IL-1 γ polypeptide sequence.
SEQ ID NO: 9 provides primate IL-1 β polypeptide sequence.
SEQ ID NO: 10 provides rodent IL-1 β polypeptide sequence.
SEQ ID NO: 11 provides primate IL-1RA polypeptide sequence.
SEQ ID NO: 12 provides rodent IL-1RA polypeptide sequence.
15 SEQ ID NO: 13 provides rodent IL-1 δ polypeptide sequence.
SEQ ID NO: 14 provides rodent IL-1 ϵ polypeptide sequence.
SEQ ID NO: 15 provides primate IL-1 ϵ polypeptide sequence.

20 (1) GENERAL INFORMATION:

(i) APPLICANT: Timans, Jacqueline C.

25 (ii) TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and
Methods

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

30 (A) ADDRESSEE: DNAX Research Institute
(B) STREET: 901 California Avenue
(C) CITY: Palo Alto
(D) STATE: California
(E) COUNTRY: USA
35 (F) ZIP: 94304-1104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
40 (B) COMPUTER: Apple Macintosh
(C) OPERATING SYSTEM: Macintosh 8.5.1
(D) SOFTWARE: Microsoft Word

(vi) CURRENT APPLICATION DATA:

45 (A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: DX0904K

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 491..1144

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGTTTGTTT TCTTTAGAGA TTTTACAGTG TTGTTATAA TTGTGCACTT AATCTTTATT 60
TTCCTTATAC AGTAGTCCCC CCGATCAACT GGGGGCATGT TCCATACCCC TGGTGGATTC 120
20 CTGAAACTGC CAGTTAGTAC CAAACCCTAT ATAGATTGTG TTTTTCCTG TACGCAGGCC 180
GACACACAGG AAATCATAAG TCAGGAGGGC CACTGCCACG CAGGAAAGAC CCATCTGAAC 240
TGCTGCAAAA GCTCCGTGTC GATTTATTGC TTCCACAAAT AGTGCCGATA TGCACCAGGC 300
25 ACTGTTGTAA AACTGAAAAT ATGTTTTGGG ATGTGCCAG TCTACCTAGC TCCTTCAAGT 360
AAAGGATCCT GAGAACTGAA GGCAACAGA GCTCCAGGAG TCCAAGACAG AGCCACACAC 420
30 CACGAGGATC CTGGCCCAGG TCTTGGACTT CCATTCCCAT TTCTGTTGAG TAATAAACTC 480
AACGTTGAAA ATG TCC TTT GTG GGG GAG AAC TCA GGA GTG AAA ATG GGC 529
Met Ser Phe Val Gly Glu Asn Ser Gly Val Lys Met Gly
1 5 10
35 TCT GAG GAC TGG GAA AAA GAT GAA CCC CAG TGC TGC TTA GAA GAC CCG 577
Ser Glu Asp Trp Glu Lys Asp Glu Pro Gln Cys Cys Leu Glu Asp Pro
15 20 25
40 GCT GGA AGC CCC CTG GAA CCA GGC CCA AGC CTC CCC ACC ATG AAT TTT 625
Ala Gly Ser Pro Leu Glu Pro Gly Pro Ser Leu Pro Thr Met Asn Phe
30 35 40 45
GTT CAC ACA AGT CGA AAG GTG AAG AGC TTA AAC CCG AAG AAA TTC AGC 673
45 Val His Thr Ser Arg Lys Val Lys Ser Leu Asn Pro Lys Lys Phe Ser
50 55 60
ATT CAT GAC CAG GAT CAC AAA GTA CTG GTC CTG GAC TCT GGG AAT CTC 721
Ile His Asp Gln Asp His Lys Val Leu Val Leu Asp Ser Gly Asn Leu
50 65 70 75
ATA GCA GTT CCA GAT AAA AAC TAC ATA CGC CCA GAG ATC TTC TTT GCA 769
Ile Ala Val Pro Asp Lys Asn Tyr Ile Arg Pro Glu Ile Phe Phe Ala
80 85 90
55 TTA GCC TCA TCC TTG AGC TCA GCC TCT GCG GAG AAA GGA AGT CTG ATT 817
Leu Ala Ser Ser Leu Ser Ser Ala Ser Ala Glu Lys Gly Ser Leu Ile
95 100 105

CTC CTG GGG GTC TCT AAA GGG GAG TTT TGT CTC TAC TGT GAC AAG GAT 865
 Leu Leu Gly Val Ser Lys Gly Glu Phe Cys Leu Tyr Cys Asp Lys Asp
 110 115 120 125
 5 AAA GGA CAA AGT CAT CCA TCC CTT CAG CTG AAG AAG GAG AAA CTG ATG 913
 Lys Gly Gln Ser His Pro Ser Leu Gln Leu Lys Lys Glu Lys Leu Met
 130 135 140
 10 AAG CTG GCT GCC CAA AAG GAA TCA GCA CGC CGG CCC TTC ATC TTT TAT 961
 Lys Leu Ala Ala Gln Lys Glu Ser Ala Arg Arg Pro Phe Ile Phe Tyr
 145 150 155
 15 AGG GCT CAG GTG GGC TCC CGG AAC ATG CTG GAG TCG GCG GCT CAC CCC 1009
 Arg Ala Gln Val Gly Ser Arg Asn Met Leu Glu Ser Ala Ala His Pro
 160 165 170
 GGA TGG TTC ATC TGC ACC TCC TGC AAT TGT AAT GAG CCT GTT GGG GTG 1057
 Gly Trp Phe Ile Cys Thr Ser Cys Asn Cys Asn Glu Pro Val Gly Val
 175 180 185
 20 ACA GAT AAA TTT GAG AAC AGG AAA CAC ATT GAA TTT TCA TTT CAA CCA 1105
 Thr Asp Lys Phe Glu Asn Arg Lys His Ile Glu Phe Ser Phe Gln Pro
 190 195 200 205
 25 GTT TGC AAA GCT GAA ATG AGC CCC AGT GAG GTC AGC GAT TAGGAACTG 1154
 Val Cys Lys Ala Glu Met Ser Pro Ser Glu Val Ser Asp
 210 215
 30 CCCCATTGAA CGCCTTCCTC GCTAATTTGA ACTAATTGTA TAAAAACCCC AAACCTGCTC 1214
 ACTAAAAAAA A 1225

(2) INFORMATION FOR SEQ ID NO:2:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

45 Met Ser Phe Val Gly Glu Asn Ser Gly Val Lys Met Gly Ser Glu Asp
 1 5 10 15
 Trp Glu Lys Asp Glu Pro Gln Cys Cys Leu Glu Asp Pro Ala Gly Ser
 20 25 30
 50 Pro Leu Glu Pro Gly Pro Ser Leu Pro Thr Met Asn Phe Val His Thr
 35 40 45
 55 Ser Arg Lys Val Lys Ser Leu Asn Pro Lys Lys Phe Ser Ile His Asp
 50 55 60
 Gln Asp His Lys Val Leu Val Leu Asp Ser Gly Asn Leu Ile Ala Val
 65 70 75 80

DX0904K

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(2) INFORMATION FOR SEQ ID NO:3:

30      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 657 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

35      (ii) MOLECULE TYPE: cDNA

          (ix) FEATURE:
30          (A) NAME/KEY: CDS
          (B) LOCATION: 1..654

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

45      ATG TCC TTT GTG GGG GAG AAC TCA GGA GTG AAA ATG GGC TCT GAG GAC
      Met Ser Phe Val Gly Glu Asn Ser Gly Val Lys Met Gly Ser Glu Asp
          1             5             10             15

50      TGG GAA AAA GAT GAA CCC CAG TGC TGC TTA GAA GAC CCG GCT GTA AGC
      Trp Glu Lys Asp Glu Pro Gln Cys Cys Leu Glu Asp Pro Ala Val Ser
          20             25             30

55      CCC CTG GAA CCA GGC CCA AGC CTC CCC GCC ATG AAT TTT GTT CAC ACA
      Pro Leu Glu Pro Gly Pro Ser Leu Pro Ala Met Asn Phe Val His Thr
          35             40             45

      AGT CCA AAG GTG AAG AAC TTA AAC CCG AAG AAA TTC AGC ATT CAT GAC
      Ser Pro Lys Val Lys Asn Leu Asn Pro Lys Lys Phe Ser Ile His Asp
          50             55             60

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	CAG GAT CAC AAA GTA CTG GTC CTG GAC TCT GGG AAT CTC ATA GCA GTT	240
	Gln Asp His Lys Val Leu Val Leu Asp Ser Gly Asn Leu Ile Ala Val	
	65 70 75 80	
5	CCA GAT AAA AAC TAC ATA CGC CCA GAG ATC TTC TTT GCA TTA GCC TCA	288
	Pro Asp Lys Asn Tyr Ile Arg Pro Glu Ile Phe Phe Ala Leu Ala Ser	
	85 90 95	
10	TCC TTG AGC TCA GCC TCT GCG GAG AAA GGA AGT CCG ATT CTC CTG GGG	336
	Ser Leu Ser Ser Ala Ser Ala Glu Lys Gly Ser Pro Ile Leu Leu Gly	
	100 105 110	
15	GTC TCT AAA GGG GAG TTT TGT CTC TAC TGT GAC AAG GAT AAA GGA CAA	384
	Val Ser Lys Gly Glu Phe Cys Leu Tyr Cys Asp Lys Asp Lys Gly Gln	
	115 120 125	
20	AGT CAT CCA TCC CTT CAG CTG AAG AAG GAG AAA CTG ATG AAG CTG GCT	432
	Ser His Pro Ser Leu Gln Leu Lys Lys Glu Lys Leu Met Lys Leu Ala	
	130 135 140	
25	GCC CAA AAG GAA TCA GCA CGC CGG CCC TTC ATC TTT TAT AGG GCT CAG	480
	Ala Gln Lys Glu Ser Ala Arg Arg Pro Phe Ile Phe Tyr Arg Ala Gln	
	145 150 155 160	
30	GTG GGC TCC TGG AAC ATG CTG GAG TCG GCG GCT CAC CCC GGA TGG TTC	528
	Val Gly Ser Trp Asn Met Leu Glu Ser Ala Ala His Pro Gly Trp Phe	
	165 170 175	
35	ATC TGC ACC TCC TGC AAT TGT AAT GAG CCT GTT GGG GTG ACA GAT AAA	576
	Ile Cys Thr Ser Cys Asn Cys Asn Glu Pro Val Gly Val Thr Asp Lys	
	180 185 190	
40	TTT GAG AAC AGG AAA CAC ATT GAA TTT TCA TTT CAA CCA GTT TGC AAA	624
	Phe Glu Asn Arg Lys His Ile Glu Phe Ser Phe Gln Pro Val Cys Lys	
	195 200 205	
45	GCT GAA ATG AGC CCC AGT GAG GTC AGC GAT TAG	657
	Ala Glu Met Ser Pro Ser Glu Val Ser Asp	
	210 215	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 218 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Phe Val Gly Glu Asn Ser Gly Val Lys Met Gly Ser Glu Asp
 1 5 10 15
 55 Trp Glu Lys Asp Glu Pro Gln Cys Cys Leu Glu Asp Pro Ala Val Ser
 20 25 30

Pro Leu Glu Pro Gly Pro Ser Leu Pro Ala Met Asn Phe Val His Thr
 35 40 45
 5 Ser Pro Lys Val Lys Asn Leu Asn Pro Lys Lys Phe Ser Ile His Asp
 50 55 60
 Gln Asp His Lys Val Leu Val Leu Asp Ser Gly Asn Leu Ile Ala Val
 65 70 75 80
 10 Pro Asp Lys Asn Tyr Ile Arg Pro Glu Ile Phe Phe Ala Leu Ala Ser
 85 90 95
 Ser Leu Ser Ser Ala Ser Ala Glu Lys Gly Ser Pro Ile Leu Leu Gly
 100 105 110
 15 Val Ser Lys Gly Glu Phe Cys Leu Tyr Cys Asp Lys Asp Lys Gly Gln
 115 120 125
 Ser His Pro Ser Leu Gln Leu Lys Lys Glu Lys Leu Met Lys Leu Ala
 20 130 135 140
 Ala Gln Lys Glu Ser Ala Arg Arg Pro Phe Ile Phe Tyr Arg Ala Gln
 145 150 155 160
 25 Val Gly Ser Trp Asn Met Leu Glu Ser Ala Ala His Pro Gly Trp Phe
 165 170 175
 Ile Cys Thr Ser Cys Asn Cys Asn Glu Pro Val Gly Val Thr Asp Lys
 180 185 190
 30 Phe Glu Asn Arg Lys His Ile Glu Phe Ser Phe Gln Pro Val Cys Lys
 195 200 205
 Ala Glu Met Ser Pro Ser Glu Val Ser Asp
 35 210 215

(2) INFORMATION FOR SEQ ID NO:5:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 159 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: peptide

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser Ala Pro Phe Ser Phe Leu Ser Asn Val Lys Tyr Asn Phe Met Arg
 1 5 10 15
 55 Ile Ile Lys Tyr Glu Phe Ile Leu Asn Asp Ala Leu Asn Gln Ser Ile
 20 25 30
 Ile Arg Ala Asn Asp Gln Tyr Leu Thr Ala Ala Ala Leu His Asn Leu
 35 40 45
 60

Asp Glu Ala Val Lys Phe Asp Met Gly Ala Tyr Lys Ser Ser Lys Asp
 50 55 60
 5 Asp Ala Lys Ile Thr Val Ile Leu Arg Ile Ser Lys Thr Gln Leu Tyr
 65 70 75 80
 Val Thr Ala Gln Asp Glu Asp Gln Pro Val Leu Leu Lys Glu Met Pro
 85 90 95
 10 Glu Ile Pro Lys Thr Ile Thr Gly Ser Glu Thr Asn Leu Leu Phe Phe
 100 105 110
 Trp Glu Thr His Gly Thr Lys Asn Tyr Phe Thr Ser Val Ala His Pro
 115 120 125
 15 Asn Leu Phe Ile Ala Thr Lys Gln Asp Tyr Trp Val Cys Leu Ala Gly
 130 135 140
 20 Gly Pro Pro Ser Ile Thr Asp Phe Gln Ile Leu Glu Asn Gln Ala
 145 150 155

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 156 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Ala Pro Tyr Thr Tyr Gln Ser Asp Leu Arg Tyr Lys Leu Met Lys
 1 5 10 15
 40 Leu Val Arg Gln Lys Phe Val Met Asn Asp Ser Leu Asn Gln Thr Ile
 20 25 30
 Tyr Gln Asp Val Asp Lys His Tyr Leu Ser Thr Thr Trp Leu Asn Asp
 35 40 45
 45 Leu Gln Gln Glu Val Lys Phe Asp Met Tyr Ala Tyr Ser Ser Gly Gly
 50 55 60
 50 Asp Asp Ser Lys Tyr Pro Val Thr Leu Lys Ile Ser Asp Ser Gln Leu
 65 70 75 80
 Phe Val Ser Ala Gln Gly Glu Asp Gln Pro Val Leu Leu Lys Glu Leu
 85 90 95
 55 Pro Glu Thr Pro Lys Leu Ile Thr Gly Ser Glu Thr Asp Leu Ile Phe
 100 105 110
 Phe Trp Lys Ser Ile Asn Ser Lys Asn Tyr Phe Thr Ser Ala Ala Tyr
 115 120 125
 60

Pro Glu Leu Phe Ile Ala Thr Lys Glu Gln Ser Arg Val His Leu Ala
 130 135 140

5 Arg Gly Leu Pro Ser Met Thr Asp Phe Gln Ile Ser
 145 150 155

(2) INFORMATION FOR SEQ ID NO:7:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu
 1 5 10 15

25 Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu
 20 25 30

Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe
 35 40 45

30 Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr
 50 55 60

35 Ile Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn Lys
 65 70 75 80

Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr
 85 90 95

40 Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn
 100 105 110

Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys
 115 120 125

45 Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu
 130 135 140

50 Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp
 145 150 155

(2) INFORMATION FOR SEQ ID NO:8:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Asn Phe Gly Arg Leu His Cys Thr Thr Ala Val Ile Arg Asn Ile
 1 5 10 15
 Asn Asp Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe Glu Asp
 20 25 30
 Met Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg Leu Ile
 35 40 45
 Ile Tyr Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val Thr Leu
 50 55 60
 Ser Val Lys Asp Ser Lys Met Ser Thr Leu Ser Cys Lys Asn Lys Ile
 65 70 75 80
 Ile Ser Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp Ile Gln
 85 90 95
 Ser Asp Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn Lys Met
 100 105 110
 Glu Phe Glu Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys Gln Lys
 115 120 125
 Glu Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly
 130 135 140
 Asp Lys Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser
 145 150 155

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg Asp Ser Gln Gln
 1 5 10 15
 Lys Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys Ala Leu His Leu
 20 25 30
 Gln Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser Met Ser Phe Val
 35 40 45

60

Glu His Lys Pro Val Phe Leu Gly Asn Asn Ser Gly Gln Asp Ile Ile
 130 135 140

5 Asp Phe Thr Met Glu Ser Val Ser Ser
 145 150

(2) INFORMATION FOR SEQ ID NO:11:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear.

15 (ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Cys Arg Pro Ser Gly Arg Lys Ser Ser Lys Met Gln Ala Phe Arg Ile
 1 5 10 15

25 Trp Asp Val Asn Gln Lys Thr Phe Tyr Leu Arg Asn Asn Gln Leu Val
 20 25 30

Ala Gly Tyr Leu Gln Gly Pro Asn Val Asn Leu Glu Glu Lys Ile Asp
 35 40 45

30 Val Val Pro Ile Glu Pro His Ala Leu Phe Leu Gly Ile His Gly Gly
 50 55 60

35 Lys Leu Cys Leu Ser Cys Val Lys Ser Gly Asp Glu Thr Arg Leu Gln
 65 70 75 80

Leu Glu Ala Val Asn Ile Thr Asp Leu Ser Glu Asn Arg Lys Gln Asp
 85 90 95

40 Lys Arg Phe Ala Phe Ile Arg Ser Asp Ser Gly Pro Thr Thr Ser Phe
 100 105 110

Glu Ser Ala Ala Cys Pro Gly Trp Phe Leu Cys Thr Ala Met Glu Ala
 115 120 125

45 Asp Gln Pro Val Ser Leu Thr Asn Met Pro Asp Glu Gly Val Met Val
 130 135 140

50 Thr Lys Phe Tyr Phe Gln Glu Asp Glu
 145 150

(2) INFORMATION FOR SEQ ID NO:12:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Cys Arg Pro Ser Gly Lys Arg Pro Cys Lys Met Gln Ala Phe Arg Ile
 1 5 10 15
 Trp Asp Thr Asn Gln Lys Thr Phe Tyr Leu Arg Asn Asn Gln Leu Ile
 20 25 30
 Ala Gly Tyr Leu Gln Gly Pro Asn Ile Lys Leu Glu Glu Lys Ile Asp
 35 40 45
 Met Val Pro Ile Asp Leu His Ser Val Phe Leu Gly Ile Lys Gly Tyr
 50 55 60
 Lys Leu Tyr Met Ser Cys Val Lys Ser Gly Asp Asp Ile Lys Leu Gln
 65 70 75 80
 Leu Glu Glu Val Asn Ile Thr Asp Leu Ser Lys Asn Lys Glu Glu Asp
 85 90 95
 Lys Arg Phe Thr Phe Ile Arg Ser Glu Lys Gly Pro Thr Thr Ser Phe
 100 105 110
 Glu Ser Ala Ala Cys Pro Gly Trp Phe Leu Cys Thr Thr Leu Glu Ala
 115 120 125
 Asp Arg Pro Val Ser Leu Thr Asn Thr Pro Glu Glu Pro Leu Ile Val
 130 135 140
 Thr Lys Phe Tyr Phe Gln Glu Asp Gln
 145 150

(2) INFORMATION FOR SEQ ID NO:13:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear
 45 (ii) MOLECULE TYPE: peptide

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Met Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala
 1 5 10 15
 Leu Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu
 20 25 30
 His Ala Glu Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn
 35 40 45

60

Arg Ala Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly
 50 55 60
 5 Gly Ser Gln Cys Leu Ser Cys Gly Thr Glu Lys Gly Pro Ile Leu Lys
 65 70 75 80
 Leu Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser
 85 90 95
 10 Lys Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe
 100 105 110
 Glu Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Ser Pro Glu Ala
 115 120 125
 15 Asp Gln Pro Val Arg Leu Thr Gln Ile Pro Glu Asp Pro Ala Trp Asp
 130 135 140
 Ala Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
 145 150 155
 20

(2) INFORMATION FOR SEQ ID NO:14:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 160 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Asn Lys Glu Lys Glu Leu Arg Ala Ala Ser Pro Ser Leu Arg His
 1 5 10 15
 40 Val Gln Asp Leu Ser Ser Arg Val Trp Ile Leu Gln Asn Asn Ile Leu
 20 25 30
 Thr Ala Val Pro Arg Lys Glu Gln Thr Val Pro Val Thr Ile Thr Leu
 35 40 45
 45 Leu Pro Cys Gln Tyr Leu Asp Thr Leu Glu Thr Asn Arg Gly Asp Pro
 50 55 60
 50 Thr Tyr Met Gly Val Gln Arg Pro Met Ser Cys Leu Phe Cys Thr Lys
 65 70 75 80
 Asp Gly Glu Gln Pro Val Leu Gln Leu Gly Glu Gly Asn Ile Met Glu
 85 90 95
 55 Met Tyr Asn Lys Lys Glu Pro Val Lys Ala Ser Leu Phe Tyr His Lys
 100 105 110
 Lys Ser Gly Thr Thr Ser Thr Phe Glu Ser Ala Ala Phe Pro Gly Trp
 115 120 125
 60

Phe Ile Ala Val Cys Ser Lys Gly Ser Cys Pro Leu Ile Leu Thr Gln
 130 135 140

5 Glu Leu Gly Glu Ile Phe Ile Thr Asp Phe Glu Met Ile Val Val His
 145 150 155 160

(2) INFORMATION FOR SEQ ID NO:15:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 169 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala Val Tyr
 1 5 10 15

25 Gln Ser Met Cys Lys Pro Ile Thr Gly Thr Ile Asn Asp Leu Asn Gln
 20 25 30

30 Gln Val Trp Thr Leu Gln Gly Gln Asn Leu Val Ala Val Pro Arg Ser
 35 40 45

Asp Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys Tyr Pro
 50 55 60

35 Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln
 65 70 75 80

Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro Thr
 85 90 95

40 Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln Pro Glu
 100 105 110

45 Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg Thr Ser
 115 120 125

Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser Ser Lys
 130 135 140

50 Arg Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu Gly Lys Ser Tyr Asn
 145 150 155 160

Thr Ala Phe Glu Leu Asn Ile Asn Asp
 165

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